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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 08:34:56 2000; MasPar time 21.20 Seconds 659.132 Million cell updates/sec

Tabular output not generated.

Title:

Description:
Perfect Score:
Sequence: >US-09-331-631-8 (1-590) from US09331631.pep (1 of 4) 4332 1 MVRNKSACVVLLFSLFLSFG.....FNSNPQESYFVSRQRQRASE 590

Scoring table:

PAM 150 Gap 11

Searched:

188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35 1:geneseqp

Statistics: Mean 36.568; Variance 172.610; scale 0.212

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	<sub>U</sub>	4	ω	2	_	Result No.
130	136	138		, 143	147	190	716	737	758	764	761	784	834	834	955	966	1236	1244	1246	1910	2101	4332	Score
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00	0 00	186	515	351	1382	395	444	524	637	489	409	626	614	614	593	605	666	625	666	525	566	590	
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W 9 0 / 0	W95073	W26536	R47128	R24393	W31867	W03474	W90340	W90339	W62837	W90341	W90342	W22150	W62834	W22149	W62835	W62838	W62829	W62830	W62828	W62831	R20181	W62832	ID
GST-HD lusion protein	GST-HD fusion protein	Trypanosoma cruzi anti	Oat globin A2B.	Sequence of Histidine-	Human metastasis-assoc	Mouse SRY-related prot	G. max truncated SBP1	G. max SBP1 protein.	Hordeum vulgare antimi	G. max SBP2 protein.	G. max truncated SBP2	Peanut allergen Ara hI	Arachis hypogaea antim	Peanut allergen Ara hI	Zea mays antimicrobial	Glycine max antimicrob	Macadamia integrifolia	Macadamia integrifolia	Macadamia integrifolia	Theobroma cacao antimi	~	Gossypium hirsutum ant	Description
1./3e-U1	1.73e-01	1.25e-01	6.43e-02	5.45e-02	.79e	.65e-	4.48e-50	6.35e-52	8.97e-54	2.65e-54	.88e-5	4.56e-56	က်	. 73	ż	.32e-7	2.50e-96			4.54e-157	2.30e-174	0.00e+00	Pred. No.

136 3.1 94 1 W95080 GST-HD fusion protein 136 3.1 94 1 W95075 GST-HD fusion protein 134 3.1 561 1 P61333 Soybean glycinin A5A4B 133 3.1 562 1 R70491 Leucocytozoan protezoan 132 3.0 472 1 R47127 Modified oat globin A2 125 2.9 499 1 P82755 Rice storage protein 126 2.9 1529 1 R97885 CORK potassium channel 127 2.8 96 1 W99822 HIV A30S protein sequence of 128 2.8 108 1 W95071 Amino acid sequence of 129 2.8 167 1 W89768 Amino acid sequence of 129 2.8 167 1 W89768 Staphylococcus aureus 129 2.8 167 1 W89768 Staphylococcus aureus 129 2.8 737 1 R76639 Deltex protein Produce 123 2.8 737 1 R76639 Deltex protein 120 2.8 1132 1 R97866 Colicken Leucocytozoan 120 2.8 134 W31866 Mouse metastasis-association 120 2.7 2237 1 R71006 Human calcium 121 2.7 2237 1 R73106 Human calcium 121 2.7 233 1 R33549 Sequence of the alpha	45	44	43	42	41	40	39	38	37	36	35 5	34	ω ω	32	31	30	29	28	27	26	25	24
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1 W95080 1 W95075 1 P61163 1 R47127 1 R827255 1 R27749 1 R27749 1 W95071 1 W95071 1 W95071 1 W95071 1 W85768 1 W85162 1 W18317 1 W18317 1 W18317 1 W18317 1 R76640 1 R76640 1 R334666 1 R33449	2.7	2.7	2.7	2.7	2.8	۷. 8	2.8	2.8	2.8	2.8	2.8	2.8	2.8	8	2.9	2.9	2.9	3.0	3.1	3.1	ω. μ	ω
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GST-HD fusion protein GST-HD fusion protein GST-HD fusion protein Soybean glycinin A5AAB Leucocytozoan protozoa Modified oat globin A2 Rice storage protein CORK potassium channel Human calcium channel HIV A30s protein seque Amino acid sequence of Amino acid sequence of Staphylococcus aureus Soybean glycinin A3B4 Drosophila Deltex prot Deltex protein produce Deltex protein Chicken leucocytozoan Mouse metastasis-assoc Peptide fragment of N- Human neuronal calcium Sequence of the alpha	R33549	R71006	W63142	R96420	W31866	R97866	R76640	R76639	W18317	P61362	W89768	W95076	W95071	W99832	R27649	R97985	P82755	R47127	R70491	P61363	W95075	W95080
	Sequence of the alpha	Human neuronal calcium	Human calcium channel	Peptide fragment of N-	Mouse metastasis-assoc	Chicken leucocytozoan	Deltex protein.	Deltex protein produce	Drosophila Deltex prot	Soybean glycinin A3B4	Staphylococcus aureus	Amino acid sequence of	Amino acid sequence of	HIV A30S protein seque	Human calcium channel	CORK potassium channel	Rice storage protein.	Modified oat globin A2	Leucocytozoan protozoa	Soybean glycinin A5A4B	fusion	-HD fusion

## ALIGNMENTS

g	Qy Db	Qy Db	Оy	Qy Db	Qy Db	¥ B Q	HRESULT POR REPORT OF THE SULT
301 NPGQFEEFFPAGSQRPQSYLRAFSREILEPAFNTRSEQLDELFGGRQSRRRQQGQGMFRK 360	241 KIYLVTNGRGTLTFLTHENKESYNIVPGVVVKVPAGSTVYLANQDNKEKLIIAVLHRPVN 300 	181 PFHFHRRSEQSREREEHGNFRVLQRFASRHPILRGINEFRLSILEANPNTFVLPHHCDAE 240 	121 QRQFQECQOHCHQQEQRPEKKQQCVRECREKYQENPWRGEREEEAEEEETEEGEQEQSHN 180 	61 CEESCKSQYGEKDQQQRHRPEDPQRRYEECQQECRQQEERQQPQCQQRCLKRFEQEQQQS 120 	1 MVRNKSACVVLLFSLFLSFGALCSAKDFPGRRGDDDPPKRYEDCRRRCEWDTRGQKEQQQ 60	Query Match 100.0%; Score 4332; DB 1; Length 590; Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 590; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	W62832 standard; Protein; 590 AA. W62832; W62832; W62832; 27-OCT-1998 (first entry) 27-OCT-1998 (first entry) antimicrobial protein; infestation; control. Gossypium hirsutum. GOSSYPIUM hirsutum. W6287805-A1. 02-JUL-1998. 02-DEC-1997; AU0874. 02-DEC-1997; AU0874. 02-DEC-1997; AU0874. 02-DEC-1997; AU0874. 03-DEC-1997; AU0874. 04-DEC-1997; AU0874. 05-DEC-1997; AU0874. 06-DEC-1997; AU0874. 07-DEC-1998-377279/32. MFI; 98-377279/32. Novel anti-microbial protein from e.g. Macadamia integrifolia - useful for controlling microbial infestations of plants or mammals Claim 1; Page 49-51; 96pp; English. The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammalian animals. Sequence 590 AA;

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(Claim 4; Fig 2; 59pp; English.

(Claim 4; Fig 2; 59pp; English.

The inventors claim a 67 kD and 31 kD T. cacao protein, and fragments, and encoding DNAs. The 47 kD and 31 kD proteins are derived from the 67 kD precursor. T. cacao protein cDNA was detected in a cDNA library prepared from immature cocoa beams RNA using a probe based on the AA sequence of a CNBr peptide common to the 47 kD and 31 kD polypeptides. Homology searches revealed close homologies between the 67 kD polypeptide and the vicilins, which are
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11-JUN-1990; GB-013016.
(MRSC ) MARS UK LTD.
Spencer ME, Hodge R, Deakin
MPI: 92-024418/03.
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02-JUL-1998.
22-DEC-1997;
20-DEC-1996;
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20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPIC
Bower NI, Goulter KC, Green
WPI; 98-377279/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel anti-microbial protein from e.g. Macadamia integruseful for controlling microbial infestations of plants Claim 1, Page 47-49, 96pp; English.

The sequence is that of an antimicrobial protein which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9827805-A1.
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KAPLSPGDVFVAPAGHAVTFFASKDQPLNAVAFGLNAQN
                                                                                                                                                                                                                                                                                                                  DSEAKELSFGVPSKLVDNIFN-NPDESYFMSFSQQRQRRDE
||:|||:|||:||| | |
| DSQAKELAFGVSSRLVDEIFNSNPQESYFVS--RQRQRASE
                                                                                                      VPHYNSKATFVVFVTDGYGYAQMACPHLSRQSQGSQSGRQDRREQEEESEEETFGEFQQV
                                                                                                                                                EATSPREKSGERFAFNLLSQTPRYSNQNGRFFEACPPEFRQLRDINVTVSALQLNQGSIF
                                                                                                                                                                        QATSPRHRGGERLAINLLSQSPVYSNQNGRFFEACPEDFSQFQNMDVAVSAFKLNQGAIF
                                                                                                                                                                                                                                                          FRDEEGNFKILQRFAENSPPLKGINDYRLAMFEANPNTFILPHHCDAEAIYFVINGKGTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPRQQYEQCQRRCESEATEEREQEQCEQRCEREYKEQQRQQEEELQRQYQQCQGRCQEQQ
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                                                                VPHYNSKATFVILVTEGNGYAEMVSPHLPRQSSYEEEEEEEDEEEEQEQEEERRSGQYRKI
                                                                                                                                                                                                                                  SQRPQSYLRAFSREILEPAFNTRSEQLDELFGGRQSRRRQQGQ-GMFRKASQEQIRALSQ
                                                                                                                                                                                                                                                                                                                                                                                                        FREEHGNFRVLQRFASRHPILRGINEFRLSILEANPNTFVLPHHCDAEKIYLVTNGRGTL
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261; Conser
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llarity 56.9%;
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Pred. No. 4.54e-157;
95; Mismatches 92:
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AETR-) COOP RES CENT TRO.

BOWER NI, GOULTER KC, Gree.

WPI; 98-377279/32.

N-PSDB; V42310.

Novel anti-mi-

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Best Local Similarity
Matches 223; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel anti-microbial protein from e.g. Macadamia integruseful for controlling microbial infestations of plants Claim 1; Page 34-36; 96pp; English.

The sequence is that of an antimicrobial protein which be used to control microbial infestations in plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macadamia integrifolia antimicrobial antimicrobial protein; infestation;
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   VEESFNSQDQSIFFPGPRQHQQQS
                                                                                                                                                                                                                                                                                                     PAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDEEK----YEER-MKEEDNKRDPQQREYEDCRRRCEQQEPRQQ--HQCQLRCREQQRQH ::|: :: | | | | | | : :| | | | | | | :::
                                                                                      PVVFVSSGNENLLLFAFGINAQN-N--H-EN-FLAGRERNVLQQIEPQAMELAFAAPRKE
                                                                                                                                                        GEADVEMACPHL---SG--RHGGRGGGKRHEEEED--V-HYEQVRARLSKREAIVVLAGH
                                                                                                                                                                                                        LLSQTPRYSNQNGRFFEACPPEFRQLRDINVTVSALQLNQGSIFVPHYNSKATFVILVTE
                                                                                                                                                                                                                                                                                   TRSEQLDELFGGRQSRRRQQGQGMFRKASQEQIRALSQEATSPRE----KSGE--RFAFN
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                                                                                                                                 GNGYAEMVSPHLPRQSSYEEEEEEDEEEEQEQEEEERRSGQYRKIRSRLSRGDIFVVPANF
                                                                                                                                                                                                                                                                                                                                                       PAGSTYYLANQDNKEKLI IAVLHRPVNNPGQFEEFFPAGSQRPQSYLRAFSREILEPAFN
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                                                         PVTFVASQNQNLRMTGFGLYNQNINPDHNQRIFVAGKINHV-RQWDSQAKELAFGVSSRL
                                                                                                                                                                                                                                             LFNKRPLYSNKYGQAYEVKPEDYRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVVAS
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29. .666
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39.5%;
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Pred. No. 3.18e-97;
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, Manners JM, Marcus
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Best Local :
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Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel anti-microbial protein from e.g. Mac useful for controlling microbial infestati Claim 1; Page 43-45; 96pp; English. The sequence is that of an antimicrobial pe used to control microbial infestations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bower NI, Goulter KC, WPI; 98-377279/32.
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22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macadamia integrifolia antimicrobial antimicrobial protein; infestation;
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27-OCT-1998
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VEELFNSQDESIFFPGPRQHQQQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNGYAEMVSPHLPRQSSYEEEEEEEDEEEEQEQEEEERRSGQYRKIRSRLSRGDIFVVPANF
                                                                                                                                                                    GEADVEMACPHL - - -
                                                                                                                                                                                                                             LFNKRPLYSNKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVAS
                                                                                                                                                                                                                                                                                TRSEQLDELFGGRQSRRRQQGQGMFRKASQEQIRALSQEAT-SPR-E--KSGE--RFAFN
                                                                                                                                                                                                                                                                                                                  TQTERLRGVLG--Q--QRE-G-VIIR-ASQEQIRELTRDDSESRRWHIRRGGESSRGPYN 415
                                                                                                                                                                                                                                                                                                                                                                              PAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALN 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RALKNYRLVLLEANPNAFYLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PWRGE-REEEAEEEET-EEGEQEQSHNPFHFHRRSFQSRFREEHGNFRVLQRFASRHPIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRGGDLMNPQRGGSGRYEEGEEKQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQEERQQPQCQQRCLKRFEQEQQQSQRQFQECQQHCHQQEQRPEKKQQCVRECREKYQEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDEEK----YEER-MKEGDNKRDPQQREYEDCRRHCEQQEPRLQ--YQCQRRCQEQQRQH 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPPKRYEDCRRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQRHRPEDPQRRYEECQQECR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VDEIFNSNPQESYFVS-RQRQRAS
                                                                                                                                                                                                        LLSQTPRYSNQNGRFFEACPPEFRQLRDINVTVSALQLNQGSIFVPHYNSKATFVILVTE
                                                                                                                                                                                                                                                                                                                                                       PAGSTVYLANQDNKEKLIIAVLHRPVNNPGQFEEFFPAGSQRPQSYLRAFSREILEPAFN
                                                                                                                                                                                                                                                                                                                                                                                                                                  RGINEFRLSILEANPNTFVLPHHCDAEKIYLVTNGRGTLTFLTHENKESYNIVPGVVVKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 28.7%;
Similarity 39.9%;
225; Conservative
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                                                                                                                                                                  -SG--RHGGRGGGKRHEEEEE--V-HYEQVRARLSKREAIVVLAGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1244; DB 1; I
Pred. No. 4.80e-97;
149; Mismatches 143;
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s in plants and mar
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RESULTANT RESULT
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Best Local Similarity 39.4%;
Matches 222; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel anti-microbial protein from e.g. Macadamia integrifolia useful for controlling microbial infestations of plants or man Claim 1; Page 39-41; 96pp; English.

The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RETR-) COOP RES CENT TROPICAL BOWER NI, Goulter KC, Green JL, WPI; 98-377279/32.
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22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
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27-OCT-1998
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     VEELFNSQDESIFFPGPRQHQQQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TQAERLRGVLG--Q--QRE---GVIISASQEQIRELTRDDSESRRWHIRRGGESSRGPYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDEEK----YEER-MKEEDNKRDPQQREYEDCRRCCEQQEPRQQ--YQCQRRCREQQRQH 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPQQQYEQCQERCQRHETEPRHMQTCQQRCERRY-EKEK--R-K-Q--QKRYEE-QQ--R 170
                                                                                         PVTFVASQNQNLRMTGFGLYNQNINPDHNQRIFVAGKINHV-RQWDSQAKELAFGVSSRL
                                                                                                                       GNGYAEMVSPHLPRQSSYEEEEEEDEEEEQEQEEEERRSGQYRKIRSRLSRGDIFVVPANF
                                                                                                                                                                                                                                                                 GEADVEMACPHL - - - SG - RHGGRRGGKR - HEEEED - - V - HYEQVKARLSKREAIVVPVGH
                                                                                                                                                                                                                                                                                                                         LLSQTPRYSNQNGRFFEACPPEFRQLRDINVTVSALQLNQGSIFVPHYNSKATFVILVTE
                                                                                                                                                                                                                                                                                                                                                       LENKRPLYSNKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                           TRSEQLDELFGGRQSRRRQQGQGMFRKASQEQIRALSQEAT-SPR-E--KSGE--RFAFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAGSTVYLANQDNKEKLIIAVLHRPVNNPGQFEEFFPAGSQRPQSYLRAFSREILEPAFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALN 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQEERQQPQCQQRCLKRFEQEQQQSQRQFQECQQHCHQQEQRPEKKQQCVRECREKYQEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPPKRYEDCRRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQRHRPEDPQRRYEECQQECR
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  standard;
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29. .666
/note= "mature n
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pred. No. 2.50e-96;
151; Mismatches 144
                                      647
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22-DEC-1996; AU-004275.
20-DEC-1996; AU-004275.
20-DEC-1996; AU-004275.
RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
WPI; 98-377279/32.
Novel anti-microbial protein from e.g. Macadamia integrifol useful for controlling microbial infestations of plants or Claim 1; Page 63-65; 96pp; English.
The sequence is that of an antimicrobial protein which can be added to the control of the
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168; Mismatches 164
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                                               29-DEC-1997 (first entry)
Peanut allergen Ara hI.
Peanut seed storage protein; allergen; allergy; hypersensitivity;
vaccine; anaphylactic shock; immunotherapy; therapy;
monoclonal antibody; ELISA; analysis; Ara hI.
Arachis hypogaea strain Florunger.
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02-JUL-1998.
22-DEC-1997; AUO874.
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                                                                                                                                                     W22149 standard; Protein; 614 W22149;
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The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammalian
 Protein
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Zea mays antimicrobial protein.
antimicrobial protein; infestation; control
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                                                                                                                                                                                                                                    QESYF
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                                                                                                                                                                                                                                                                                                                                                                                                                         FEACPPEFROLRDINVTVSALQLNQGSIFVPHYNSKATF-VILVTEGNGYAEMVSPHLPR
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172; Conser
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 /label= Sig_peptide
23. .614
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Pred. No. 3.17e-71;
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Claim 31; Page 169; 354pp; English.

Claim 31; Page 169; 264pp; English.

Claim 31; Page 169; 264pp; English.

Claim 31; Page 169; 264pp; English.

Claim 31; Page 169; 354pp; English.

Claim 31; Page 169; 264pp; English.

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Best Local
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10-JUL-1997.
23-SEP-1996; U15222.
04-MAR-1996; US-610424.
29-DEC-1995; US-009455.
(UVAR-) UNIV ARKANSAS.
Bannon GA, Burks AW, C
WPI; 97-363453/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; T76612
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                          EKLIK-NQRESHFVSARPQSQS
                                                                                                                    VAINAS-SE-LHLLGFG-----INAENNHRIFLAGDKDNVIDQIEKQAKDLAFPGSGEQV
                                                                                                                                                                                                           TGNLELVAVRKEQQQR-GRREQEWEEEEEEDEEEEGSNREVRRYTARLKEGDVFIMPAAHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGYAEMVSPHLPRQSSYEEEEEEEDEEEEQEQEEERRSGQYRKIRSRLSRGDIFVVPANFP
                                                                                                                                                                                                                                                                           SQTPRYSNONGRFFEACPPE-FROLRDINVTVSALQLNQGSIFVPHYNSKATFVILVTEG
                                                                                                                                                                                                                                                                                                        DGEPDLSNNFGRLFEVKPDKKNPQLQDLDMMLTCVEIKEGALMLPHFNSKAMVIVVVNKG
                                                                                                                                                                                                                                                                                                                                                                       LFGG----R-QSRR--RQ-QGQGMFRKASQEQIRALSQEATSPREK-SGER-FA--FNLL
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Pred. No. 1.73e-60;
137; Mismatches 153;
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RESULT ID W

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                                              Peanut allergen Ara hI.

Peanut; seed storage protein; allergen; allergy; hypersensitivity; vaccine; anaphylactic shock; immunotherapy; therapy; monoclonal antibody; ELISA; analysis; Ara hI.

Arachis hypogaea strain Florunner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
BOWER NI, Goulter KC, Green JL, Manners JM, Marcus JP;
WPI; 98-377279/32.
Novel anti-microbial protein from e.g. Macadamia integrifolia -
                                                                                                                                                                                                                    W22150;
29-DEC-1997
                                                                                                                                                                                                                                                                              W22150 standard; Protein; 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for controlling microbial infestations of plants or mammal. Claim 1; Page 55-57; 96pp; English.
The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antimicrobial pro
Arachis hypogaea.
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27-OCT-1998
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02-JUL-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQTPRYSNQNGRFFEACPPE-FRQLRDINVTVSALQLNQGSIFVPHYNSKATFVILVTEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAGGEQEERGQRRRSTRSSDNEGVIVKVSKEHVQELTKHAKSVSKKGSEEEDITNPINLR 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPNTLVLPKHADADNILVIQQGQATVTVANGNNRKSFNLDEGHALRIPSGFISYILNRHD 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEEGE-QEQ-SHN-PFHFHRRSFQSRFREEHGNFRVLQRFASRHPILRGINEFRLSILEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEQEQQQSQRQFQECQQHCHQQE-QRPEKKQQCVRECREKYQENPWRGEREE-EAEEE-E 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGNLELVAVRKEQQQR-GRREQEWEEEEEEDEEEEGSNREVRRYTARLKEGDVFIMPAAHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEKLIIAVLHRPVNNPGQFEEFFPAGSQRPQSYLRAFSREILEPAFNTR-SE--Q--LDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPNTFVLPHHCDAEKIYLVTNGRGTLTFLTHENKESYNIVPGVVVKVPAGSTVYLANQDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               614 AA;
                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
gaea antimicrobial protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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1. .22
/label=
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Sig_peptide
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              834; DB 1;
No. 1.73e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            control
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N-PSDS; 776613.

R-PSDS; 776613.

Preanut allergens Ara hI and Ara hII - used for vaccination and in Prtwo-site monoclonal antibody based ELISA

Claim 31; Page 172; 334pp; English.

CC This polypeptide comprises major peanut allergen Ara hI (W22149).

CC Its sequence was deduced from CDNA clone P41b (T76613), isolated CC from peanut seed cDNA using a primer (see T76616) based on an isolated Ara hI peptide (see W24206). The sequence shows isolated Ara hI peptide (see W24206). The sequence shows significant homology with the vicilin family of seed storage croteins of other legumes. The allergen is recognised by serum CC significant homology with and Ara hII (see W24164) can be used to raise monoclonal antibodies which are used in a specific two-site CC waccines to protect against allergic reactions to peanut allergens, e.g. anaphylactic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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(UYAR-) UNIV ARKANSAS.
Bannon GA, Burks AW,
WPI; 97-363453/33.
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23-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167
                                                                                                           SNPQESYFVSRQRQRASE
                                                                                                                                                                                                                                     WYSPHLPRQSSYEEEEEEDEEEEQEQEEERRSGQYRKIRSRLSRGDIFVVPANFPVTFVA
                                                                                                                                                                                                                                                                                                                   LSNNFGKLFEVKPDKKNPQLQDLDMMLTCVEIKEGALMLPHFNSKAMVIVVVNKGTGNLE
                                                                                                                                                                     SQNQNLRMTGFGLYNQNINPDHNQRIFVAGKINHVR-QWDSQAKELAFGVSSRLVDEIFN
                                                                                                                                                                                       S-SE-LHLLGFG-----INAENNHRIFLAGDKDNVIDQIEKQAKDLAFPGSGEQVEKLIK
                                                                                                                                                                                                                                                                    LVAVRKEQQQR-GRREEEEDEDEEE-EGSNR--EVRRYTARLKEGDVFIMPAAHPVAINA
                                                                                                                                                                                                                                                                                                                                                                                            ERGQRRWSTRSSENNEGVIVKVSKEHVEELTKHAKSVSKKGSEEEGDITNPINLREGEPD
                                                                                                                                                                                                                                                                                                                                                                                                                             VLHRPVNNPGQFEEFFPAGSQRPQSYLRAFSREILEPAFNTR-SE--Q--LDELFGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KISMPVTQPGQFEDFFPASSRDQSSYLQGFSRNTLEAAFNAEFNEIRRVLLEENAGGEQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKHADADNILVIQQGQATVTVANGNNRKSFNLDEGHALRIPSGFISYILNRHDNQNLRVA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQEQSHNPFHFHRRSFQSRFREEHGNFRVLQRFASRHPILRGINEFRLSILEANPNTFVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EETSRNNPFYFPSRRFSTRYGNQNGRIRVLQRFDQRSRQFQNLQNHRIVQIEAKPNTLVL
                                                                                                                                        -NQKESHFVSARPQSQSQ
                                                                                                                                                                                                                                                                                                   YSNQNGRFFEACPPE-FRQLRDINVTVSALQLNQGSIFVPHYNSKATFVILVTEGNGYAE
                                                                                                                                                                                                                                                                                                                                                                 -R-QSRR--R--QQGQGMFRKASQEQIRALSQEATSPREK-SGERFAF-N-L-LSQT-PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHHCDAEKIYLVTNGRGTLTFLTHENKESYNIVPGVVVKVPAGSTVYLANQDNKEKLIIA
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18.1%;
159; Conservat
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US-009455.
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/label= Ma
521. .523
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                                                                                                                                     592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 784; DB 1;
Pred. No. 4.56e-56;
117; Mismatches 129
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                                                                                                                                                                                                      575
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W90342; W90342;

standard;

protein;

409

A

24-MAY-1999 (first e. G. max truncated SBP2

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RESULT
ID WS
AC WS
DT 2.4
DE G.
KW SG
KW SG
OS GI
PN WG
PD 26
PP 21
PR 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP. The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be desirable where it is an advantage to increase the carbohydrate content of the seed (e.g. where the seed is the primary plant material harvested, such as soybean). In contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any
                                                                        SBP1; sucrose binding protein; SBP2; seed; carbohydrate content; soybean. Glycine max.
26-NOV-1998.
21-MAY-1998; U10465.
22-MAY-1997; US-047568
                                                                                                                                                                  W90341 standard; W90341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a novel sucrose binding protein, SBP2 isol from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New modified plant sucrose binding proteins - used to transgenic plants which can have enhanced or decreased uptake activity in developing seeds Claim 7; Page 39-40; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chao ws, Grimes HD; WPI; 99-070155/06.
                                                       WO9853086-A1.
                                                                                                                                                24-MAY-1999
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(UNIW ) UNIV WASHINGTON STATE RES FOUND
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21-MAY-1998; U10465
22-MAY-1997; US-047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant; seed; carbohydrate content; soybean.
                                                                                                                                                                                                                                                                                                                                    347
                                                                                                                                                                                                                                                             405
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                                                                                                                             max SBP2 protein
                                                                                                                                                                                                                                                           ACPPEFRQ-LRDINVTVSALQLNQGSIFVPHYNSKATFVILVTEGNGYAEMVSPHLPRQS
                                                                                                                                                                                                                                                                                          VGPDDEKSWLQRLNLMLTFTNITQRSMSTIHYNSHATKIALVMDGRGHLQISCPHMSSRS
                                                                                                                                                                                                                                                                                                                                                       QN----EG-SIF-KISRERVRALAPTKKSSWWPFGGESKAQFNIFSKRPTFSNGYGRLTE
|: :| ::| | ::| | :| | |: |
                                                                                                                                                                                                                                                                                                                                                                                                      NEKLLLAMLHIPVSTPGKFEEFFGPGGRDPESVLSAFSWNVLQAALQTPKGKLERLFN-Q 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPNTFVLPHHCDAEKIYLVTNGRGTLTFLTHENKESYNIVPGVVVKVPAGSTVYLANQDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EHQEQHEEEEDENPYVFEEDKDFSTRVETEGGSIRVLKKFTEKSKLLQGIENFRLAILEA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKRFEQEQQQSQRQFQECQQHCHQQEQRPEK-KQQCVRECREKYQENPWRGEREE-EAEE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGKLKETEVEEDPELVTCKHQCQQQRQYTESDKRTCLQQCDSMKQEREKQVEEETREKEE
                                                                                                                                                                                                                                                                                                                                  QSRRRQQGQGMFRKASQEQIRALSQEATSPR-EKSGE-RFAFNLLSQTPRYSNQNGRFFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAHTFVSPRHFDSEVVLFNIKGRAVLGLVRESETEKITLEPGDMIHIPAGTPLYIVNRDE 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EETEEGEQEQSHNPFHFHR-RSFQSRFREEHGNFRVLQRFASRHPILRGINEFRLSILEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
128; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              max
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larity 35.6%;
Conservative
                                                                                                                                                (first entry)
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                                                                                                                                                                                     protein;
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Pred. No. 4.88e-54
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                                                                                                            sucrose uptake;
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                                                                                                            transgenic
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                                                                                                          plant
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RESULT
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AC WE
DT 27
DE HE
KW HE
OS HE
PN WE
PD 0:
PPF 2:
PFR 2:

Hordeum vulgare.

T 14 W62837 standard;

Protein;

637

A

antimicrobial protein; infestation; control

Hordeum vulgare antimicrobial protein.

27-OCT-1998 (first entry)

WO9827805-AĬ. 02-JUL-1998. 22-DEC-1997; AU0874. 20-DEC-1996; AU-004275

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC This sequence represents a novel sucrose binding protein, SBP2 isolated CC from Glychne max. This protein is used in a method resulting in the CC production of a modified plant sucrose binding protein (SBP) which has a CC modified amino acid sequence compared to a corresponding wild type SBP, CC and where expression of the modified SBP in a yeast assay system confers cenhanced sucrose uptake compared to the corresponding wild type SBP. CC The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be CC desirable where it is an advantage to increase the carbohydrate content of the seed (e.g. where the seed is the primary plant material harvested, such as soybean). In contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant is carbohydrate. The SBP regulatory regions confer specific or enhanced conversed. The SBP regulatory regions confer specific or enhanced conversed in developing seeds and so may be used to express any
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WPI; 99-070155/06
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Claim 13b; Page 37-38; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAHTFVSPRHFDSEVVLFNIKGRAVLGLVRESETEKITLEPGDMIHIPAGTPLYIVNRDE
FGLYNQNINPDHNQRIFVAGKINHVRQWDSQAKELAFGVSSRLVDEIFNSNPQESYF
                                                IC-FEVNVR-DNKKFTF-AGKDNIVSSLDNVAKELAFNYPSEMVNGVSERK-ESLFF 474
                                                                                                                                                                                                                                     VGPDDEKSWLQRLNLMLTFTNITQRSMSTIHYNSHATKIALVMDGRGHLQISCPHMSSRS
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                                                                                                SYEEEEEEDEEEEQEQEEERRSGQYRKIRSRLSRGDIFVVPANFPVTFVASQNQNLRMTG
                                                                                                                                                                                                                                                                                   QSRRRQQGQGMFRKASQEQIRALSQEATSPR-EKSGE-RFAFNLLSQTPRYSNQNGRFFE
                                                                                                                                                                                                                                                                                                                            QN----EG-SIF-KISRERVRALAPTKKSSWWPFGGESKAQFNIFSKRPTFSNGYGRLTE
                                                                                                                                                                                                                                                                                                                                                                                                                          NEKLLLAMLHIPVSTPGKFEEFFGPGGRDPESVLSAFSWNVLQAALQTPKGKLERLFN-Q
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161; Conser
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33.8%;
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Pred. No. 2.65e-54;
129; Mismatches 154
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                                                                                                                                                o. max SBP1 protein.
SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant; seed; carbohydrate content; soybean.
Glycine max.
26-NOV-1998.
21-MAY-1998; U10465.
22-MAY-1997; US-047568.
(UNIW ) UNIV WASHINGTON
                                                                                                                              W09853086-A1.
                                                                                                                                                                                                                                                                                                      W90339 standard; protein; W90339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for controlling microbial infestations of plants Claim 1; Page 60-62; 96pp; English.
The sequence is that of an antimicrobial protein which
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197; Conserva+'-
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Pred. No. 8.97e-54;
l65; Mismatches 205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a novel sucrose binding protein, SBP1 isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a commodified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP.

Compared to the corresponding transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be desirable where it is an advantage to increase the carbohydrate content of the seed (e.g. where the seed is the primary plant material harvested. The seed is in the vegetative material of the plant is seeds might be desirable where the vegetative material of the plant is carbose the carbohydrate content in the seed in the primary plant material of the plant is seeds might be desirable where the vegetative material of the plant is carbose the carbony in developing seeds and so may be used to express any transgene in developing seeds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 17.0%;
Best Local Similarity 34.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uptake activity in developing seeds
Disclosure; Page 34-36; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transgenic plants which can have enhanced or decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New modified plant sucrose binding proteins - used to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
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                          MVNGVF 481
                                                                                                                                                                                                                                                                                                                                                                                              AALQTPKGKLENVFD-QQN----EG-SIFR-ISREQVRALAPTKKSSWWPFGGESKPQFN 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHPFVTTASNKENLLMICFEV---N-ARDNKKFTF-AGKDNIVSSLDNVAKELAFNYPSE 475
                                                                                                                                                                                                                     IDGRGHLQISCPHMSSRSSH-----S----K-HD--KSSPSYHRISSDLKPGMVFVVPP 420
                                                                                                                                                                                                                                                                                                       IFSKRPTISNGYGRLTEVGPDDDEKSWLQRLNLMLTFTNITQRSMSTIHYNSHATKIALV 373
                                                                                                                                                                                                                                                                                                                                                                   PAFNTRSEQLDELFGGRQSRRRQQGQGMFRKASQEQIRALSQEATSPR-EKSGE-RFAFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLQGIENFRLAILEARAHTEVSPRHEDSEVVFFNIKGRAVLGLVSESETEKITLEPGDMI 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEEES-R-EREEE-QQEQ-HE-EQDENPYIFE-EDKDFETRVETEGGRIRVLKKFTEKSK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRQQE-ERQQPQCQQRCLKRFEQEQQQSQRQFQECQQHCHQ-QEQRPEKKQQCVRECREK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CKETEVEEEDPE-LVTCKHQCQQQQQYTEGDKRVCLQSCDRYHRMKQEREKQIQEETREK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WS, Grimes HI
99-070155/06
LVDEIF
                                                                                        NEPVTEVASQNQNLRMTGFGLYNQNINPDHNQRIFVAGKINHVRQWDSQAKELAFGVSSR 565
                                                                                                                                                                                 TEGNGYAEMVSPHLPRQSSYEEEEEEEDEEEEQEQEEEERRSGQYRKIRSRLSRGDIFVVPA
                                                                                                                                                                                                                                                                        LLSQTPRYSNQNGREFEACPPEF-RQ-LRDINVTVSALQLNQGSIFVPHYNSKATFVILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILRGINEFRLSILEANPNTFVLPHHCDAEKIYLVTNGRGTLTFLTHENKESYNIVPGVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YQENPWRGEREEEAEEEETEEGEQEQSHNPFHFHRRSFQSRFREEHGNFRVLQRFASRHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  524 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 737; DB 1;
Pred. No. 6.35e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                        445
                                                                                                                                                                                                                                                                                                                                                                   387
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Search completed: Sat May 13 08:35:22 Job time: 26 secs.

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